Full wwPDB X-ray Structure Validation Report (i)

Aug 27, 2023 – 09:02 AM EDT

PDB ID	:	3IIU
Title	:	Structure of the reconstituted Peridinin-Chlorophyll a-Protein (RFPCP) mutant N89L
Authors	:	Schulte, T.; Hofmann, E.
Deposited on	:	2009-08-03
Resolution	:	1.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

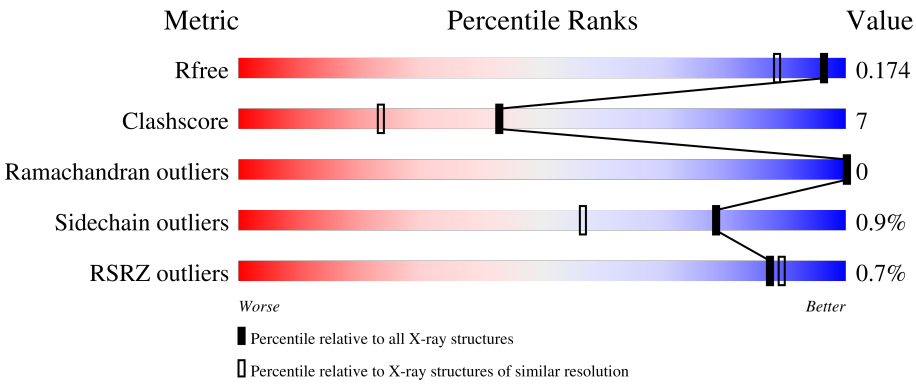
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	M	151	% 92% 7% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CLA	M	601[A]	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CLA	M	601[B]	X	-	-	-
4	J7Z	M	615[A]	X	-	-	-
4	J7Z	M	615[B]	X	-	-	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 1866 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

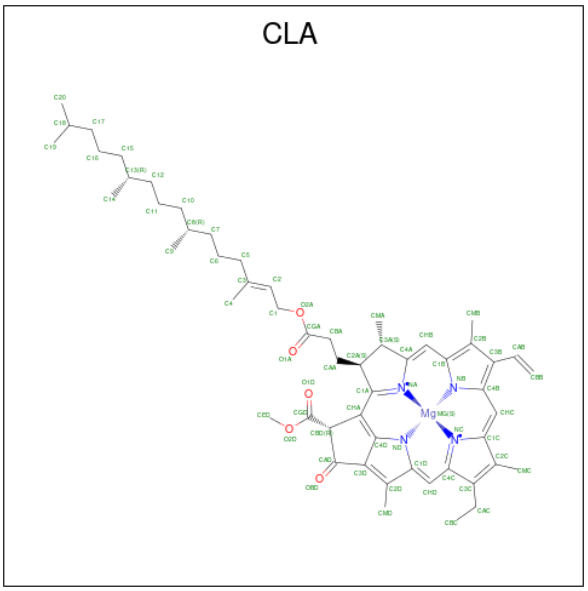
- Molecule 1 is a protein called Peridinin-chlorophyll a-binding protein 1, chloroplastic.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	M	151	1237	785	207	240	5	0	13	0

There are 3 discrepancies between the modelled and reference sequences:

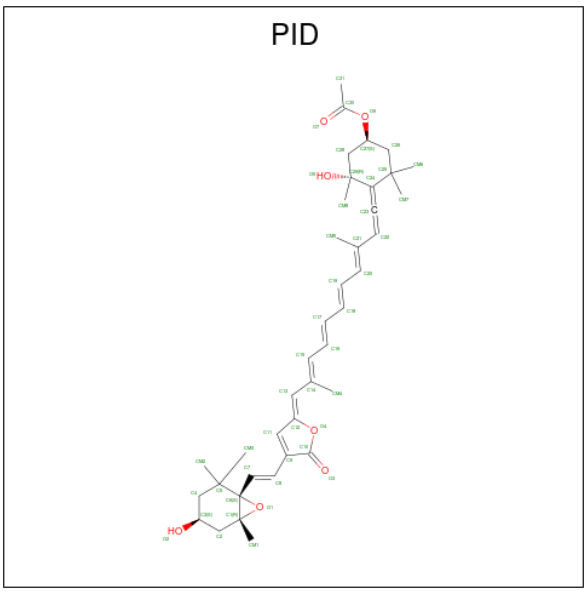
Chain	Residue	Modelled	Actual	Comment	Reference
M	87	SER	ASN	variant	UNP P80484
M	89	LEU	ASN	engineered mutation	UNP P80484
M	128	ASN	SER	variant	UNP P80484

- Molecule 2 is CHLOROPHYLL A (three-letter code: CLA) (formula: $C_{55}H_{72}MgN_4O_5$).



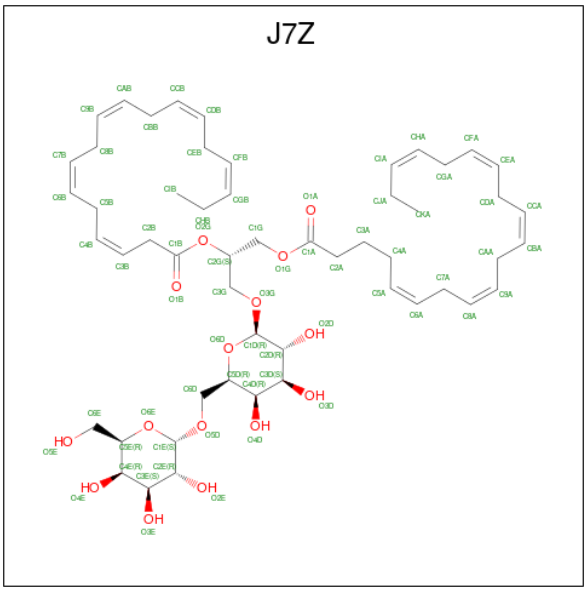
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Mg	N	O		
2	M	1	67	57	1	4	5	0	1

- Molecule 3 is PERIDININ (three-letter code: PID) (formula: $C_{39}H_{50}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	M	1	50	42	8	0	1
			Total	C	O		
3	M	1	46	39	7	0	0
			Total	C	O		
3	M	1	51	42	9	0	1
			Total	C	O		
3	M	1	46	39	7	0	0

- Molecule 4 is (2S)-3-[(6-O-alpha-D-galactopyranosyl-beta-D-galactopyranosyl)oxy]-2-[(3Z,6Z,9Z,12Z,15Z)-octadeca-3,6,9,12,15-pentaenoyloxy]propyl (5Z,8Z,11Z,14Z,17Z)-icosa-5,8,11,14,17-pentaenoate (three-letter code: J7Z) (formula: $C_{53}H_{80}O_{15}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	M	1	72	57	15	0	1

- Molecule 5 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cd		
5	M	5	6	6	0	1

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
6	M	4	4	4	0	0

- Molecule 7 is water.

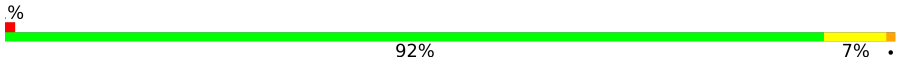
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	M	287	287	287	0	0

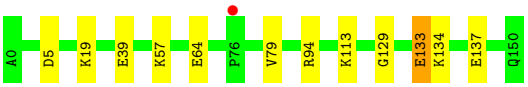
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Peridinin-chlorophyll a-binding protein 1, chloroplastic

Chain M:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	68.51Å 81.73Å 75.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.07 – 1.45 43.07 – 1.45	Depositor EDS
% Data completeness (in resolution range)	100.0 (43.07-1.45) 100.0 (43.07-1.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	4.20 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.155 , 0.176 0.153 , 0.174	Depositor DCC
R_{free} test set	1889 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	8.8	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 50.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	1866	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: CLA, CL, PID, J7Z, CD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	M	0.72	0/1257	0.79	3/1691 (0.2%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	M	5	ASP	CB-CG-OD1	6.00	123.70	118.30
1	M	5	ASP	CB-CG-OD2	-5.75	113.13	118.30
1	M	94	ARG	NE-CZ-NH1	5.62	123.11	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	M	1237	0	1255	18	0
2	M	67	0	6	2	0
3	M	193	0	146	0	0
4	M	72	0	14	0	0
5	M	6	0	0	1	0
6	M	4	0	0	1	0
7	M	287	0	0	7	0
All	All	1866	0	1421	21	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (21) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:M:151[B]:CD:CD	6:M:156:CL:CL	1.68	0.99
1:M:39[B]:GLU:OE2	7:M:431:HOH:O	1.90	0.90
1:M:64[A]:GLU:OE2	7:M:280:HOH:O	1.92	0.87
1:M:137[A]:GLU:OE1	7:M:408:HOH:O	2.13	0.65
1:M:19:LYS:HA	1:M:79[B]:VAL:HG21	1.85	0.57
1:M:57[B]:LYS:HD3	1:M:57[B]:LYS:C	2.24	0.57
1:M:39[A]:GLU:HG2	1:M:113[A]:LYS:HE2	1.88	0.55
1:M:57[B]:LYS:C	1:M:57[B]:LYS:CD	2.76	0.54
1:M:57[B]:LYS:CE	7:M:167:HOH:O	2.60	0.50
1:M:134[B]:LYS:HE3	7:M:187:HOH:O	2.12	0.49
1:M:134[A]:LYS:NZ	7:M:177:HOH:O	2.48	0.45
1:M:134[A]:LYS:HB3	1:M:134[A]:LYS:HE2	1.56	0.44
1:M:57[B]:LYS:HE3	7:M:167:HOH:O	2.19	0.42
1:M:129:GLY:O	1:M:133[A]:GLU:CG	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	M	163/151 (108%)	163 (100%)	0	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	M	128/114 (112%)	126 (98%)	2 (2%)	62 31

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	133[A]	GLU
1	M	133[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	PID	M	611[B]	-	41,49,49	1.23	3 (7%)	49,76,76	3.50	14 (28%)
3	PID	M	612	-	41,49,49	1.20	3 (7%)	49,76,76	3.44	13 (26%)
3	PID	M	614	-	41,49,49	1.18	3 (7%)	49,76,76	2.94	12 (24%)
3	PID	M	611[A]	-	41,49,49	1.28	3 (7%)	49,76,76	3.65	14 (28%)
2	CLA	M	601[A]	-	65,73,73	1.34	10 (15%)	76,113,113	1.66	9 (11%)
2	CLA	M	601[B]	-	65,73,73	1.34	10 (15%)	76,113,113	1.66	9 (11%)
3	PID	M	613[A]	-	41,49,49	1.10	4 (9%)	49,76,76	2.88	13 (26%)
3	PID	M	613[B]	-	41,49,49	1.16	5 (12%)	49,76,76	2.88	13 (26%)
4	J7Z	M	615[B]	-	69,69,69	0.74	2 (2%)	80,83,83	1.28	8 (10%)
4	J7Z	M	615[A]	-	69,69,69	0.74	2 (2%)	80,83,83	1.30	10 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PID	M	611[B]	-	-	0/24/93/93	0/4/4/4
3	PID	M	612	-	-	0/24/93/93	0/4/4/4
3	PID	M	614	-	-	0/24/93/93	0/4/4/4
3	PID	M	611[A]	-	-	0/24/93/93	0/4/4/4
2	CLA	M	601[A]	-	1/1/15/20	2/37/115/115	-
2	CLA	M	601[B]	-	1/1/15/20	2/37/115/115	-
3	PID	M	613[A]	-	-	0/24/93/93	0/4/4/4
3	PID	M	613[B]	-	-	0/24/93/93	0/4/4/4
4	J7Z	M	615[B]	-	1/1/13/33	9/57/97/97	0/2/2/2
4	J7Z	M	615[A]	-	1/1/13/33	10/57/97/97	0/2/2/2

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	601[A]	CLA	CHC-C1C	4.32	1.46	1.35
2	M	601[B]	CLA	CHC-C1C	4.32	1.46	1.35
3	M	611[A]	PID	C13-C12	4.10	1.47	1.36
3	M	611[B]	PID	C13-C12	4.10	1.47	1.36
3	M	612	PID	C13-C12	3.53	1.46	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	601[A]	CLA	CHD-C1D	3.51	1.45	1.38
2	M	601[B]	CLA	CHD-C1D	3.51	1.45	1.38
3	M	614	PID	C13-C12	3.50	1.46	1.36
3	M	613[B]	PID	O6-C30	3.38	1.42	1.35
3	M	613[A]	PID	O6-C30	3.25	1.42	1.35
3	M	612	PID	O3-C10	3.19	1.28	1.21
4	M	615[A]	J7Z	O2G-C1B	3.18	1.43	1.34
4	M	615[B]	J7Z	O2G-C1B	3.18	1.43	1.34
3	M	613[A]	PID	C13-C12	3.08	1.45	1.36
3	M	613[B]	PID	C13-C12	3.08	1.45	1.36
2	M	601[A]	CLA	CHD-C4C	3.00	1.46	1.39
2	M	601[B]	CLA	CHD-C4C	3.00	1.46	1.39
2	M	601[A]	CLA	OBD-CAD	2.70	1.27	1.22
2	M	601[B]	CLA	OBD-CAD	2.70	1.27	1.22
3	M	614	PID	C11-C12	-2.65	1.39	1.44
2	M	601[A]	CLA	O2D-CGD	2.60	1.39	1.33
2	M	601[B]	CLA	O2D-CGD	2.60	1.39	1.33
3	M	611[A]	PID	O1-C1	-2.58	1.42	1.46
3	M	611[B]	PID	O1-C1	-2.58	1.42	1.46
2	M	601[A]	CLA	C3D-C4D	-2.57	1.38	1.44
2	M	601[B]	CLA	C3D-C4D	-2.57	1.38	1.44
3	M	613[B]	PID	C26-C27	2.55	1.56	1.51
3	M	614	PID	O3-C10	2.52	1.26	1.21
2	M	601[A]	CLA	C1C-NC	-2.47	1.34	1.37
2	M	601[B]	CLA	C1C-NC	-2.47	1.34	1.37
2	M	601[A]	CLA	C1B-CHB	2.41	1.47	1.41
2	M	601[B]	CLA	C1B-CHB	2.41	1.47	1.41
4	M	615[A]	J7Z	O1G-C1A	2.39	1.40	1.33
4	M	615[B]	J7Z	O1G-C1A	2.39	1.40	1.33
3	M	613[A]	PID	C11-C12	-2.39	1.39	1.44
3	M	613[B]	PID	C11-C12	-2.39	1.39	1.44
2	M	601[A]	CLA	MG-ND	-2.36	2.01	2.05
2	M	601[B]	CLA	MG-ND	-2.36	2.01	2.05
3	M	613[A]	PID	O3-C10	2.25	1.26	1.21
3	M	613[B]	PID	O3-C10	2.25	1.26	1.21
3	M	611[A]	PID	O3-C10	2.19	1.26	1.21
3	M	611[B]	PID	O3-C10	2.19	1.26	1.21
2	M	601[A]	CLA	O2A-CGA	2.17	1.39	1.33
2	M	601[B]	CLA	O2A-CGA	2.17	1.39	1.33
3	M	612	PID	C2-C1	2.13	1.55	1.52

All (115) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	612	PID	O4-C12-C11	16.04	117.08	107.36
3	M	611[A]	PID	O4-C12-C11	15.59	116.81	107.36
3	M	611[B]	PID	O4-C12-C11	15.59	116.81	107.36
3	M	614	PID	O4-C12-C11	14.16	115.95	107.36
3	M	613[A]	PID	O4-C12-C11	13.00	115.24	107.36
3	M	613[B]	PID	O4-C12-C11	13.00	115.24	107.36
3	M	611[A]	PID	C12-O4-C10	-12.83	100.97	107.65
3	M	611[B]	PID	C12-O4-C10	-12.83	100.97	107.65
3	M	612	PID	C12-O4-C10	-11.54	101.64	107.65
3	M	613[A]	PID	C12-O4-C10	-8.94	103.00	107.65
3	M	613[B]	PID	C12-O4-C10	-8.94	103.00	107.65
3	M	611[A]	PID	O1-C1-C2	8.89	120.06	113.38
3	M	614	PID	C12-O4-C10	-8.73	103.11	107.65
3	M	612	PID	O1-C1-CM1	6.47	122.81	115.06
3	M	613[A]	PID	O1-C1-C2	6.40	118.19	113.38
3	M	613[B]	PID	O1-C1-C2	6.40	118.19	113.38
2	M	601[A]	CLA	C2D-C1D-ND	6.26	114.72	110.10
2	M	601[B]	CLA	C2D-C1D-ND	6.26	114.72	110.10
3	M	614	PID	O1-C1-C2	6.02	117.91	113.38
2	M	601[A]	CLA	CHD-C1D-ND	-5.90	119.03	124.45
2	M	601[B]	CLA	CHD-C1D-ND	-5.90	119.03	124.45
2	M	601[A]	CLA	C1D-ND-C4D	-5.34	102.54	106.33
2	M	601[B]	CLA	C1D-ND-C4D	-5.34	102.54	106.33
4	M	615[A]	J7Z	C3E-C4E-C5E	5.29	119.68	110.24
4	M	615[B]	J7Z	C3E-C4E-C5E	5.29	119.68	110.24
3	M	611[B]	PID	O1-C1-C2	5.29	117.36	113.38
3	M	611[A]	PID	O3-C10-C9	-5.04	125.01	130.74
3	M	611[B]	PID	O3-C10-C9	-5.04	125.01	130.74
3	M	611[A]	PID	O4-C10-C9	5.03	112.25	108.04
3	M	611[B]	PID	O4-C10-C9	5.03	112.25	108.04
3	M	612	PID	C6-C7-C8	-4.54	116.39	125.99
3	M	614	PID	O3-C10-C9	-4.41	125.72	130.74
3	M	612	PID	O1-C1-C2	4.33	116.63	113.38
3	M	612	PID	CM1-C1-C6	-4.05	115.48	122.26
3	M	611[A]	PID	C18-C17-C16	-3.97	115.98	124.81
3	M	611[B]	PID	C18-C17-C16	-3.97	115.98	124.81
3	M	613[A]	PID	O6-C27-C26	-3.84	98.02	107.59
3	M	612	PID	O4-C10-C9	3.84	111.25	108.04
3	M	612	PID	C17-C16-C15	-3.71	115.87	123.47
3	M	613[A]	PID	C6-C7-C8	-3.69	118.19	125.99
3	M	613[B]	PID	C6-C7-C8	-3.69	118.19	125.99
2	M	601[A]	CLA	C2C-C1C-NC	3.63	113.38	109.97
2	M	601[B]	CLA	C2C-C1C-NC	3.63	113.38	109.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	M	614	PID	C6-C7-C8	-3.62	118.34	125.99
2	M	601[A]	CLA	CAC-C3C-C4C	3.60	129.48	124.81
2	M	601[B]	CLA	CAC-C3C-C4C	3.60	129.48	124.81
4	M	615[A]	J7Z	O5D-C6D-C5D	-3.59	102.40	109.05
4	M	615[B]	J7Z	O5D-C6D-C5D	-3.59	102.40	109.05
3	M	611[A]	PID	C6-C7-C8	-3.55	118.48	125.99
3	M	611[B]	PID	C6-C7-C8	-3.55	118.48	125.99
3	M	611[A]	PID	CM3-C5-C4	-3.48	102.94	108.98
3	M	611[B]	PID	CM3-C5-C4	3.41	114.91	108.98
3	M	613[B]	PID	O6-C27-C28	-3.26	99.48	107.59
2	M	601[A]	CLA	C3D-C2D-C1D	-3.11	101.59	105.83
2	M	601[B]	CLA	C3D-C2D-C1D	-3.11	101.59	105.83
3	M	613[A]	PID	O4-C10-C9	3.10	110.63	108.04
3	M	613[B]	PID	O4-C10-C9	3.10	110.63	108.04
3	M	614	PID	O4-C10-C9	3.05	110.59	108.04
3	M	611[A]	PID	C8-C9-C11	-3.01	121.58	127.37
3	M	611[B]	PID	C8-C9-C11	-3.01	121.58	127.37
3	M	612	PID	C11-C12-C13	-2.98	121.74	128.34
2	M	601[A]	CLA	CMD-C2D-C1D	2.91	129.84	124.71
2	M	601[B]	CLA	CMD-C2D-C1D	2.91	129.84	124.71
3	M	611[A]	PID	C11-C12-C13	-2.84	122.06	128.34
3	M	611[B]	PID	C11-C12-C13	-2.84	122.06	128.34
3	M	611[B]	PID	CM2-C5-C4	-2.84	104.06	108.98
3	M	611[A]	PID	CM2-C5-C4	2.81	113.86	108.98
3	M	614	PID	CM1-C1-C6	-2.79	117.58	122.26
3	M	613[B]	PID	O6-C27-C26	2.71	114.35	107.59
3	M	614	PID	C18-C17-C16	-2.70	118.79	124.81
2	M	601[A]	CLA	CMB-C2B-C3B	2.70	129.73	124.68
2	M	601[B]	CLA	CMB-C2B-C3B	2.70	129.73	124.68
4	M	615[A]	J7Z	O6D-C1D-O3G	-2.64	103.73	109.97
4	M	615[B]	J7Z	O6D-C1D-O3G	-2.64	103.73	109.97
3	M	613[A]	PID	O1-C1-CM1	2.55	118.12	115.06
3	M	613[B]	PID	O1-C1-CM1	2.55	118.12	115.06
4	M	615[A]	J7Z	O6E-C5E-C4E	2.51	114.25	109.69
4	M	615[B]	J7Z	O6E-C5E-C4E	2.51	114.25	109.69
3	M	613[A]	PID	C11-C12-C13	-2.50	122.81	128.34
3	M	613[B]	PID	C11-C12-C13	-2.50	122.81	128.34
3	M	614	PID	C11-C12-C13	-2.46	122.90	128.34
3	M	612	PID	C19-C20-C21	-2.40	123.89	127.31
4	M	615[A]	J7Z	O4E-C4E-C3E	-2.34	104.94	110.35
4	M	615[B]	J7Z	O4E-C4E-C3E	-2.34	104.94	110.35
3	M	612	PID	O1-C1-C6	-2.34	57.03	58.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	M	615[A]	J7Z	C2B-C3B-C4B	-2.30	119.65	125.03
3	M	612	PID	C17-C18-C19	-2.30	119.69	124.81
4	M	615[A]	J7Z	C3G-C2G-C1G	-2.27	106.41	111.79
4	M	615[B]	J7Z	C3G-C2G-C1G	-2.27	106.41	111.79
3	M	611[A]	PID	O6-C27-C26	-2.27	101.95	107.59
3	M	611[B]	PID	O6-C27-C26	-2.27	101.95	107.59
3	M	614	PID	CM1-C1-C2	2.22	116.78	114.28
3	M	611[A]	PID	C1-C2-C3	2.20	117.10	112.75
3	M	613[A]	PID	C18-C17-C16	-2.16	120.01	124.81
3	M	613[B]	PID	C18-C17-C16	-2.16	120.01	124.81
3	M	611[B]	PID	C1-C2-C3	-2.15	108.49	112.75
3	M	613[A]	PID	C18-C19-C20	-2.15	119.07	123.47
3	M	613[B]	PID	C18-C19-C20	-2.15	119.07	123.47
3	M	613[A]	PID	C8-C9-C11	-2.14	123.27	127.37
3	M	613[B]	PID	C8-C9-C11	-2.14	123.27	127.37
3	M	614	PID	O6-C30-O7	-2.12	118.75	122.96
4	M	615[A]	J7Z	C1D-O6D-C5D	-2.12	109.53	113.69
4	M	615[B]	J7Z	C1D-O6D-C5D	-2.12	109.53	113.69
3	M	612	PID	C8-C9-C11	-2.09	123.36	127.37
3	M	613[A]	PID	C27-O6-C30	-2.08	114.01	117.90
3	M	614	PID	C18-C19-C20	-2.07	119.24	123.47
3	M	613[A]	PID	C17-C18-C19	-2.06	120.23	124.81
3	M	613[B]	PID	C17-C18-C19	-2.06	120.23	124.81
2	M	601[A]	CLA	C3C-C4C-NC	2.03	112.85	110.57
2	M	601[B]	CLA	C3C-C4C-NC	2.03	112.85	110.57
4	M	615[A]	J7Z	C3B-C2B-C1B	-2.03	106.47	112.68
4	M	615[A]	J7Z	C4E-C3E-C2E	2.00	114.32	110.82
4	M	615[B]	J7Z	C4E-C3E-C2E	2.00	114.32	110.82
3	M	611[A]	PID	O1-C1-CM1	2.00	117.46	115.06
3	M	611[B]	PID	O1-C1-CM1	2.00	117.46	115.06

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	M	601[A]	CLA	ND
2	M	601[B]	CLA	ND
4	M	615[A]	J7Z	C5E
4	M	615[B]	J7Z	C5E

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	M	615[A]	J7Z	O6E-C5E-C6E-O5E
4	M	615[B]	J7Z	O6E-C5E-C6E-O5E
4	M	615[A]	J7Z	C4E-C5E-C6E-O5E
4	M	615[B]	J7Z	C4E-C5E-C6E-O5E
4	M	615[A]	J7Z	C1B-C2B-C3B-C4B
4	M	615[A]	J7Z	C3B-C4B-C5B-C6B
4	M	615[A]	J7Z	C9B-CAB-CBB-CCB
4	M	615[A]	J7Z	CCB-CDB-CEB-CFB
4	M	615[B]	J7Z	C3B-C4B-C5B-C6B
4	M	615[B]	J7Z	C9B-CAB-CBB-CCB
4	M	615[B]	J7Z	CCB-CDB-CEB-CFB
4	M	615[A]	J7Z	CHA-CIA-CJA-CKA
4	M	615[B]	J7Z	CHA-CIA-CJA-CKA
4	M	615[A]	J7Z	O6D-C5D-C6D-O5D
4	M	615[B]	J7Z	O6D-C5D-C6D-O5D
4	M	615[A]	J7Z	C4D-C5D-C6D-O5D
4	M	615[B]	J7Z	C4D-C5D-C6D-O5D
4	M	615[A]	J7Z	CBA-CCA-CDA-CEA
4	M	615[B]	J7Z	CBA-CCA-CDA-CEA
2	M	601[A]	CLA	CAD-CBD-CGD-O2D
2	M	601[B]	CLA	CAD-CBD-CGD-O2D
2	M	601[A]	CLA	CAA-CBA-CGA-O2A
2	M	601[B]	CLA	CAA-CBA-CGA-O2A

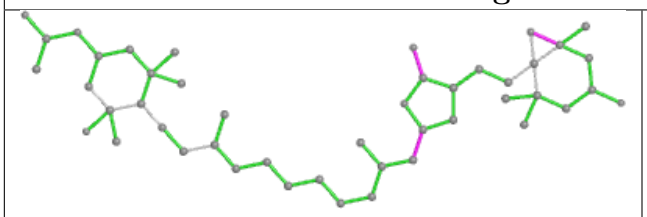
There are no ring outliers.

2 monomers are involved in 2 short contacts:

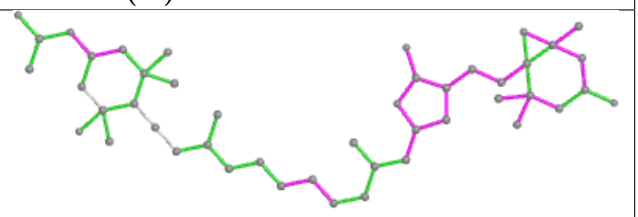
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	M	601[A]	CLA	1	0
2	M	601[B]	CLA	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

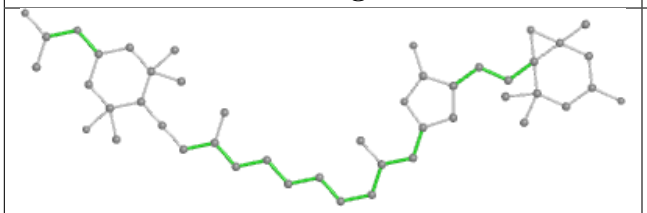
Ligand PID M 611 (B)



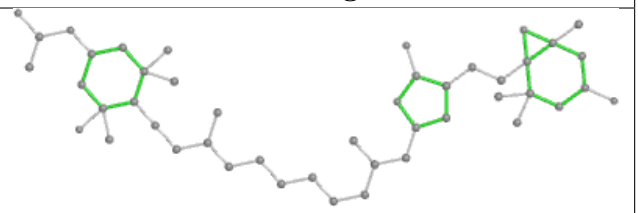
Bond lengths



Bond angles

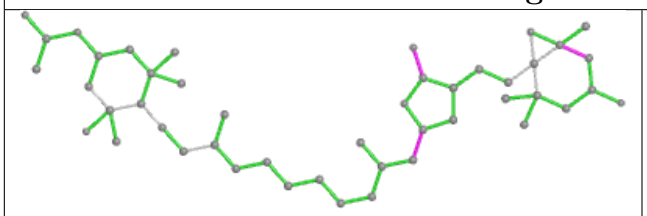


Torsions

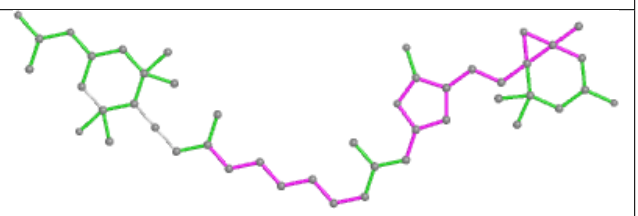


Rings

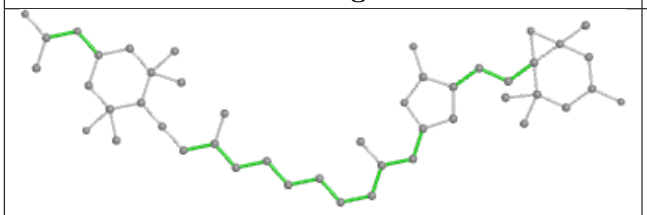
Ligand PID M 612



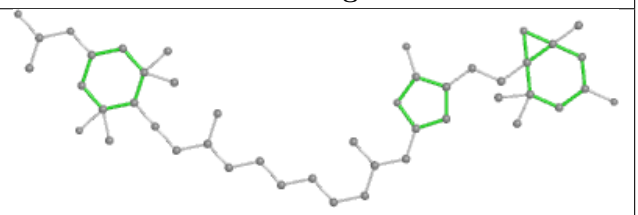
Bond lengths



Bond angles

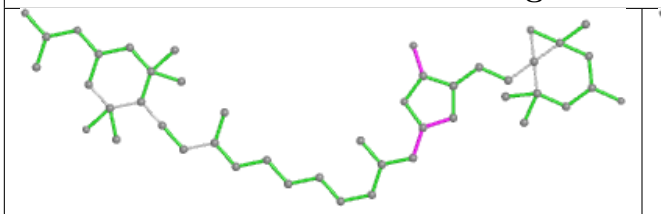


Torsions

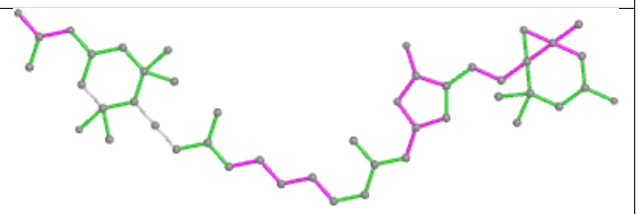


Rings

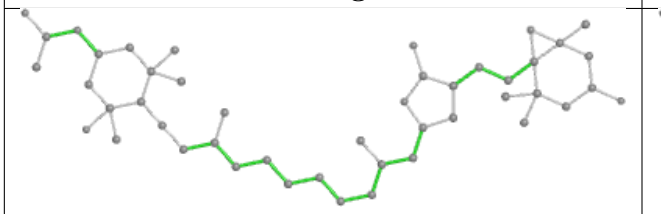
Ligand PID M 614



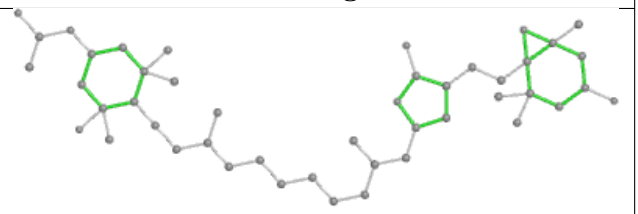
Bond lengths



Bond angles

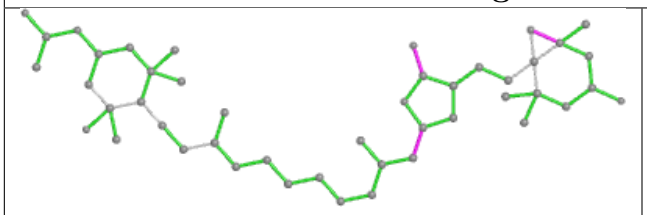


Torsions

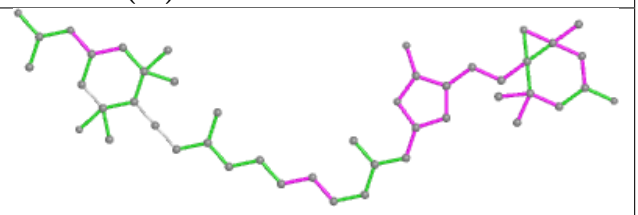


Rings

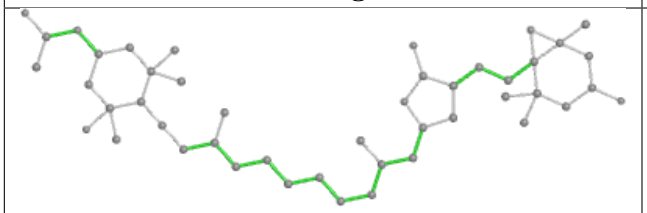
Ligand PID M 611 (A)



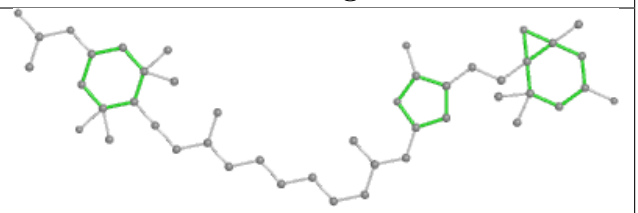
Bond lengths



Bond angles

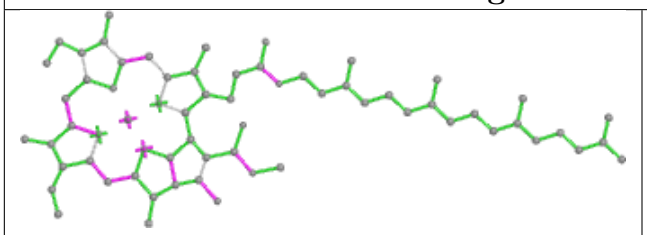


Torsions

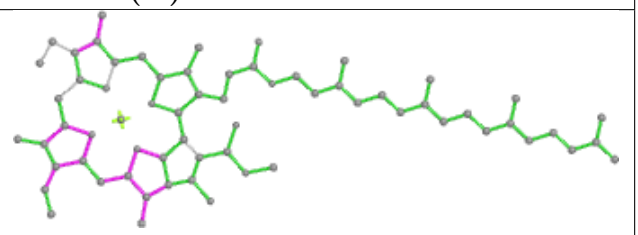


Rings

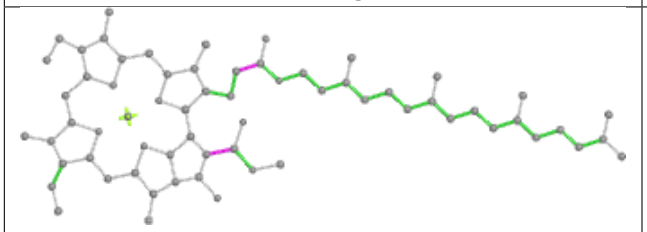
Ligand CLA M 601 (A)



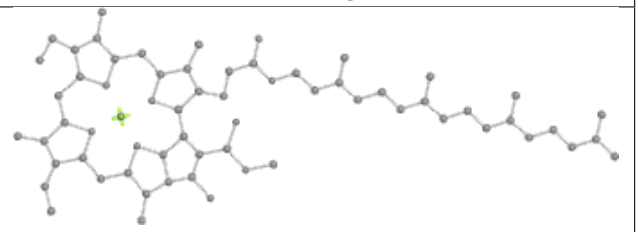
Bond lengths



Bond angles

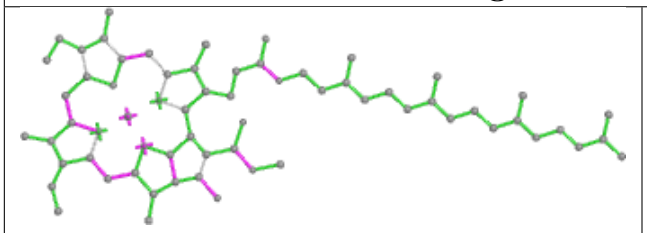


Torsions

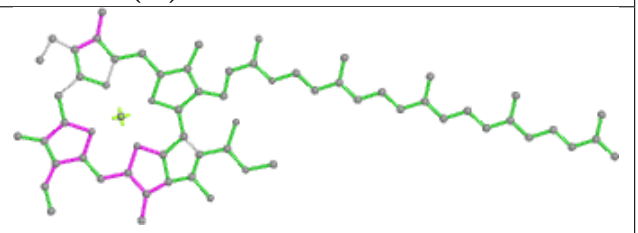


Rings

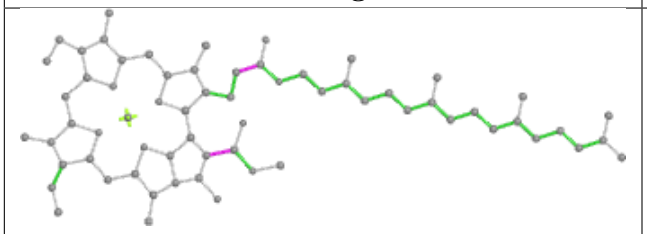
Ligand CLA M 601 (B)



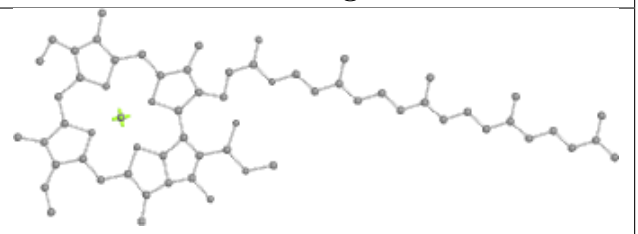
Bond lengths



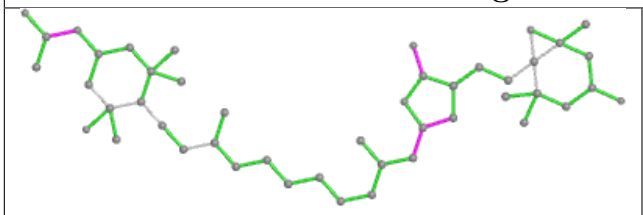
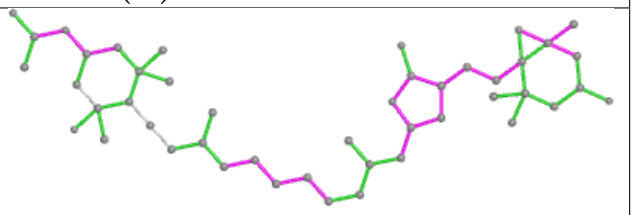
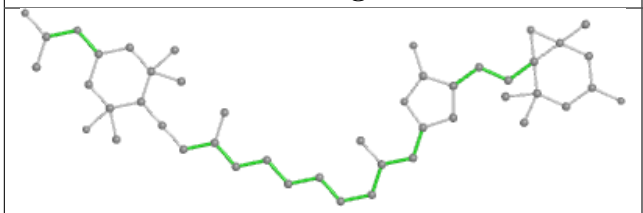
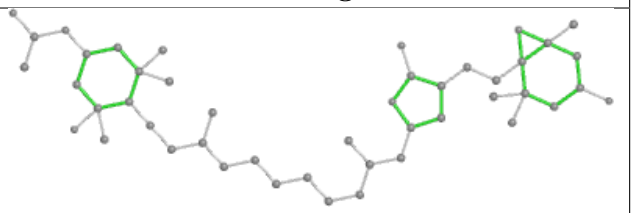
Bond angles

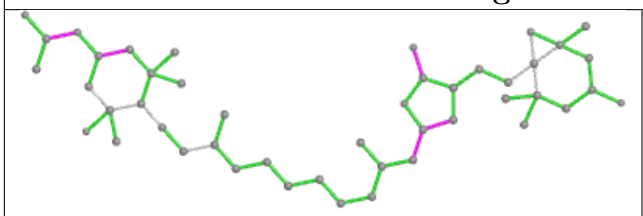
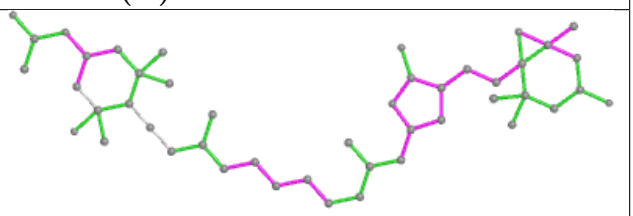
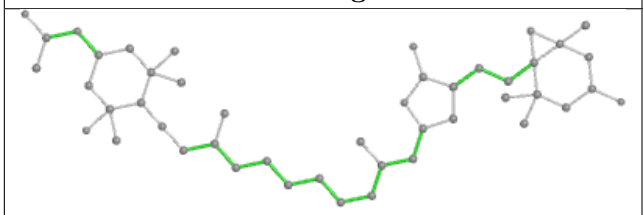
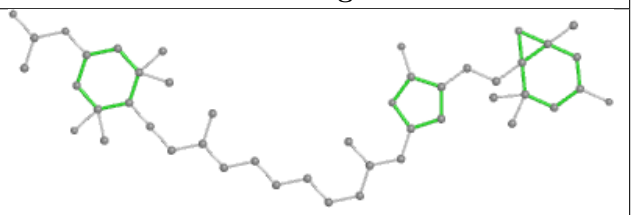


Torsions

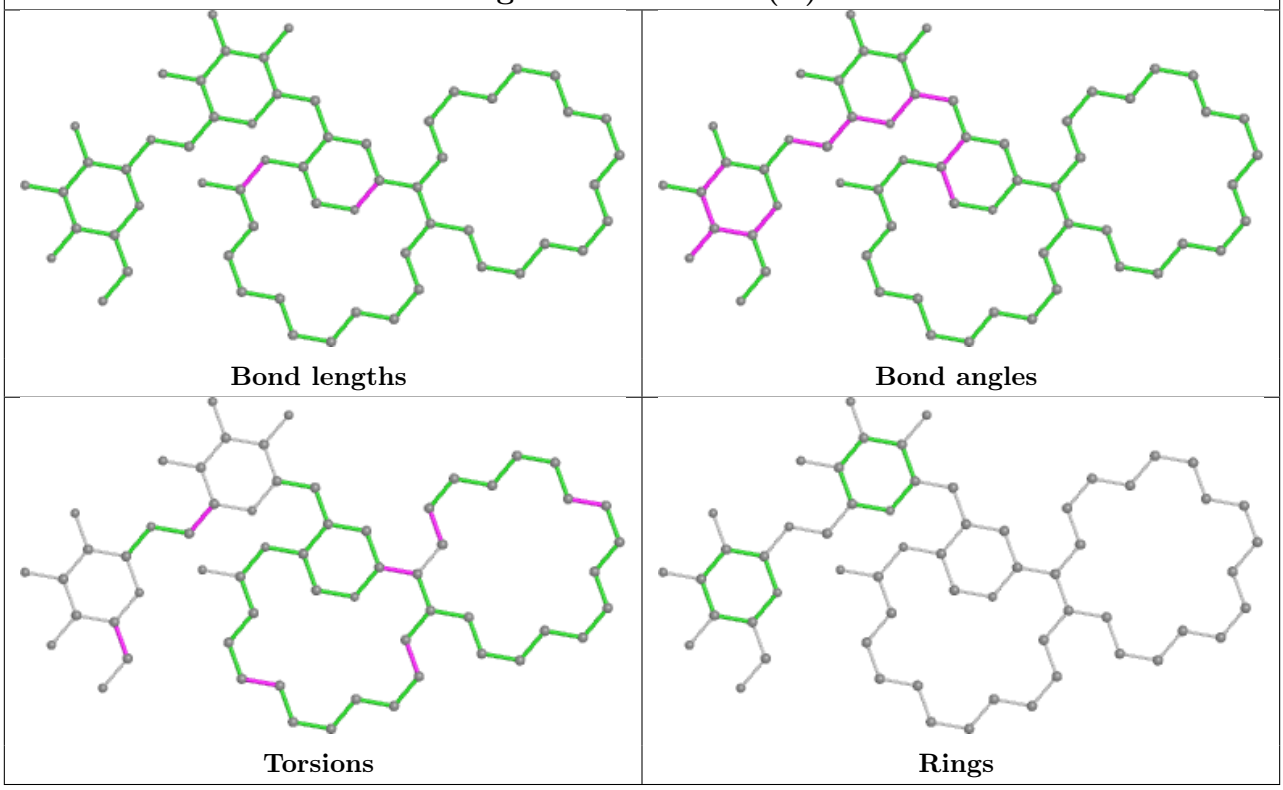


Rings

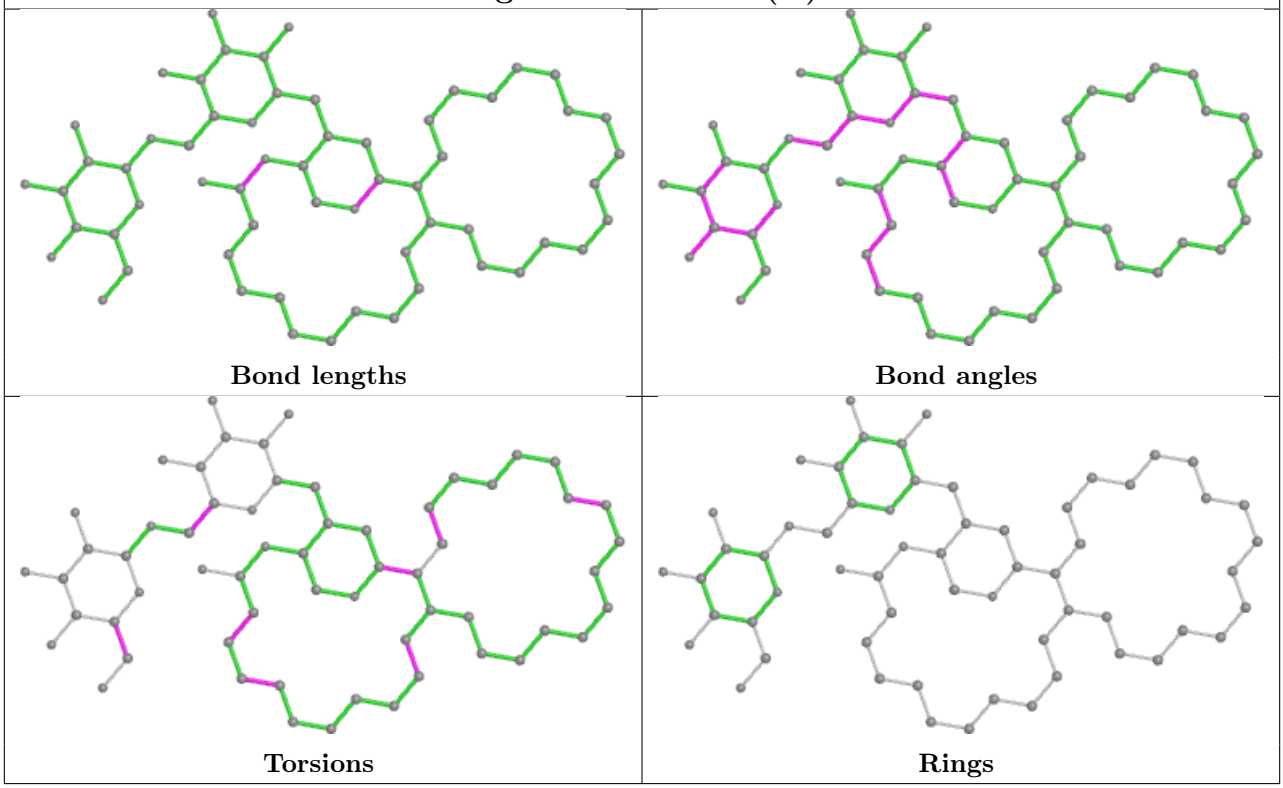
Ligand PID M 613 (A)	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand PID M 613 (B)	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand J7Z M 615 (B)



Ligand J7Z M 615 (A)



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	M	151/151 (100%)	-0.14	1 (0%)	87	89	6, 8, 15, 24	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	76	PRO	2.2

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	CL	M	156	1/1	0.86	0.14	15,15,15,15	1
4	J7Z	M	615[B]	68/68	0.91	0.12	8,14,27,29	15
4	J7Z	M	615[A]	68/68	0.91	0.12	8,14,27,29	15
3	PID	M	612	46/46	0.94	0.11	5,7,23,27	0
2	CLA	M	601[A]	65/65	0.96	0.08	3,6,9,12	2
3	PID	M	613[A]	46/46	0.96	0.09	5,7,14,19	5

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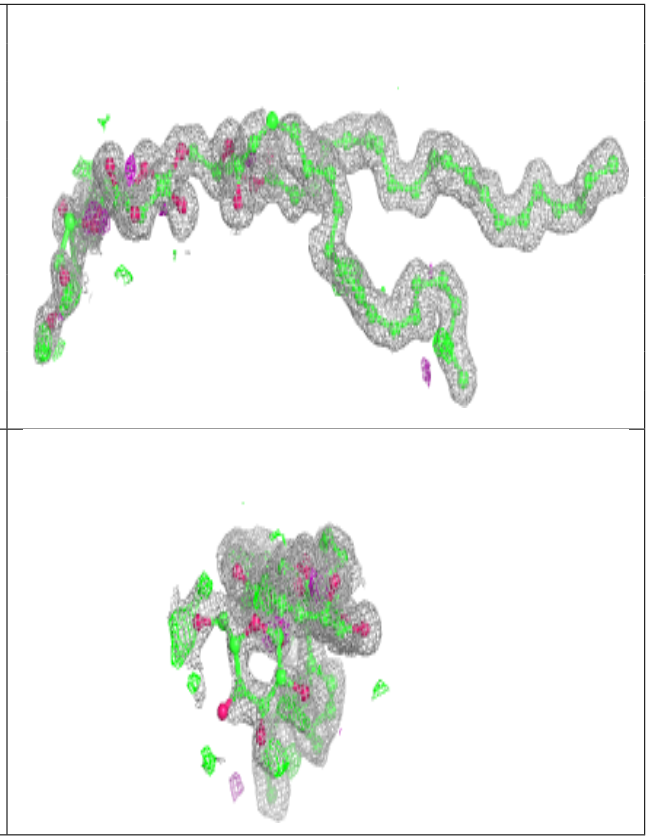
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	PID	M	613[B]	46/46	0.96	0.09	3,6,14,19	5
3	PID	M	614	46/46	0.96	0.08	4,6,8,13	0
2	CLA	M	601[B]	65/65	0.96	0.08	3,5,9,12	2
3	PID	M	611[A]	46/46	0.96	0.09	4,6,11,16	4
3	PID	M	611[B]	46/46	0.96	0.09	4,6,9,10	4
6	CL	M	157	1/1	0.98	0.06	13,13,13,13	1
5	CD	M	152	1/1	0.99	0.07	7,7,7,7	0
5	CD	M	153	1/1	0.99	0.09	8,8,8,8	1
5	CD	M	154	1/1	0.99	0.08	7,7,7,7	1
5	CD	M	155	1/1	0.99	0.09	6,6,6,6	1
5	CD	M	151[A]	1/1	0.99	0.08	8,8,8,8	1
5	CD	M	151[B]	1/1	0.99	0.08	23,23,23,23	1
6	CL	M	158	1/1	0.99	0.17	5,5,5,5	1
6	CL	M	159	1/1	1.00	0.06	6,6,6,6	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

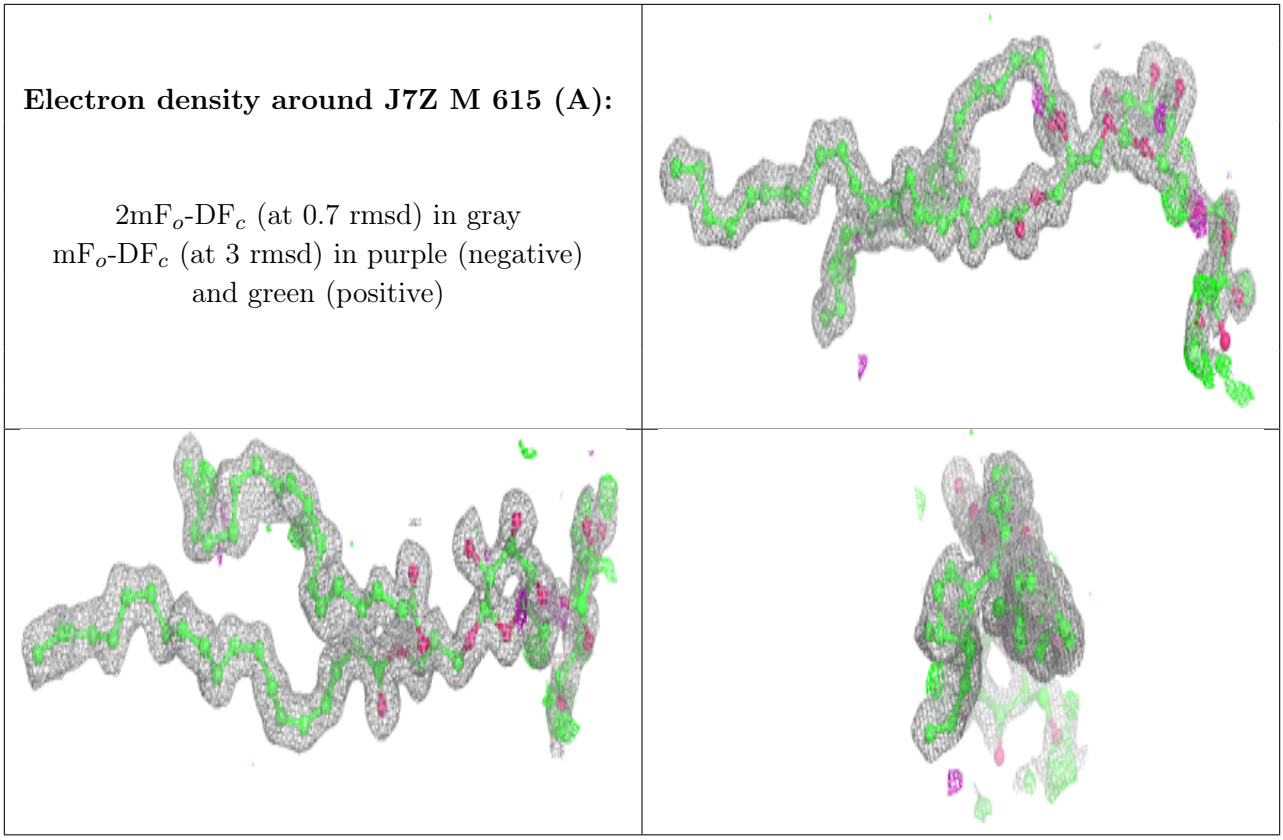
Electron density around J7Z M 615 (B):

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)



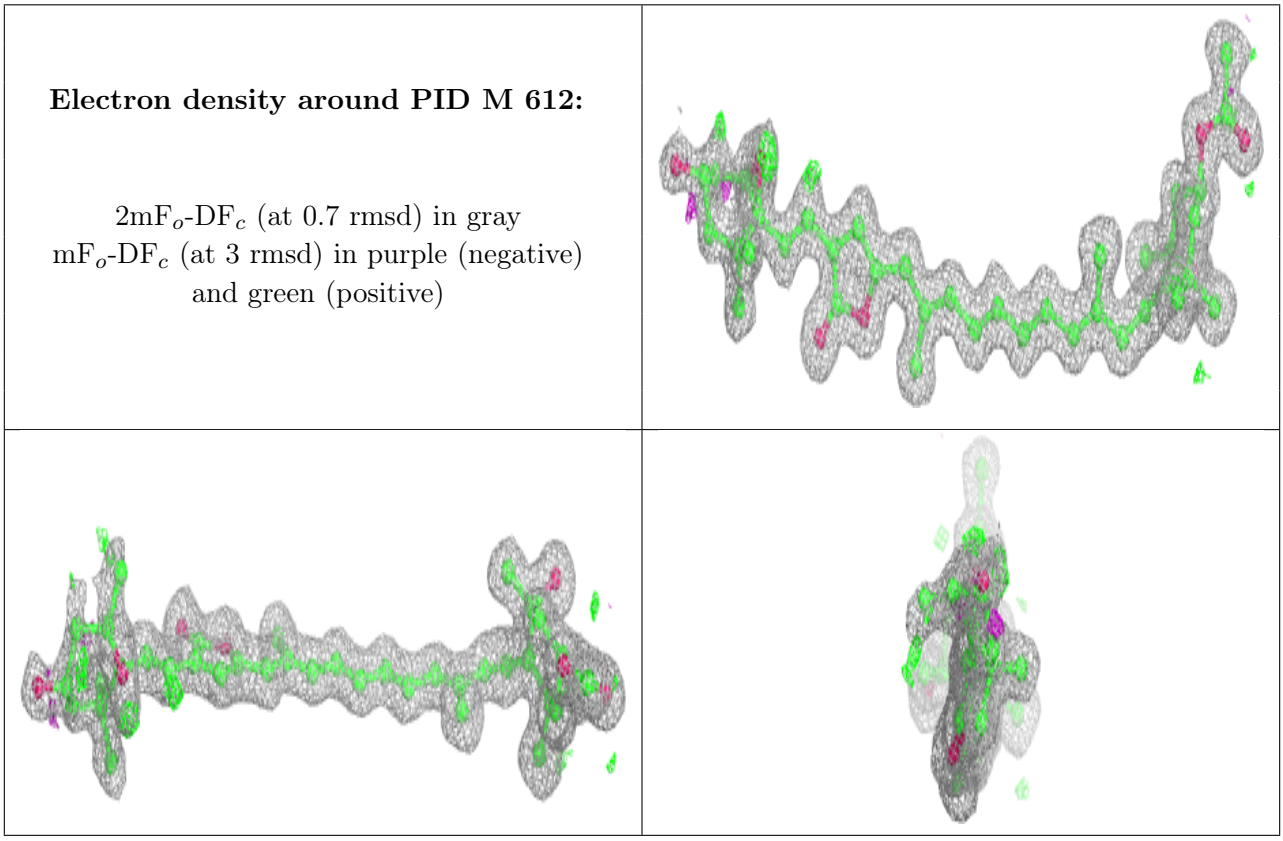
Electron density around J7Z M 615 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



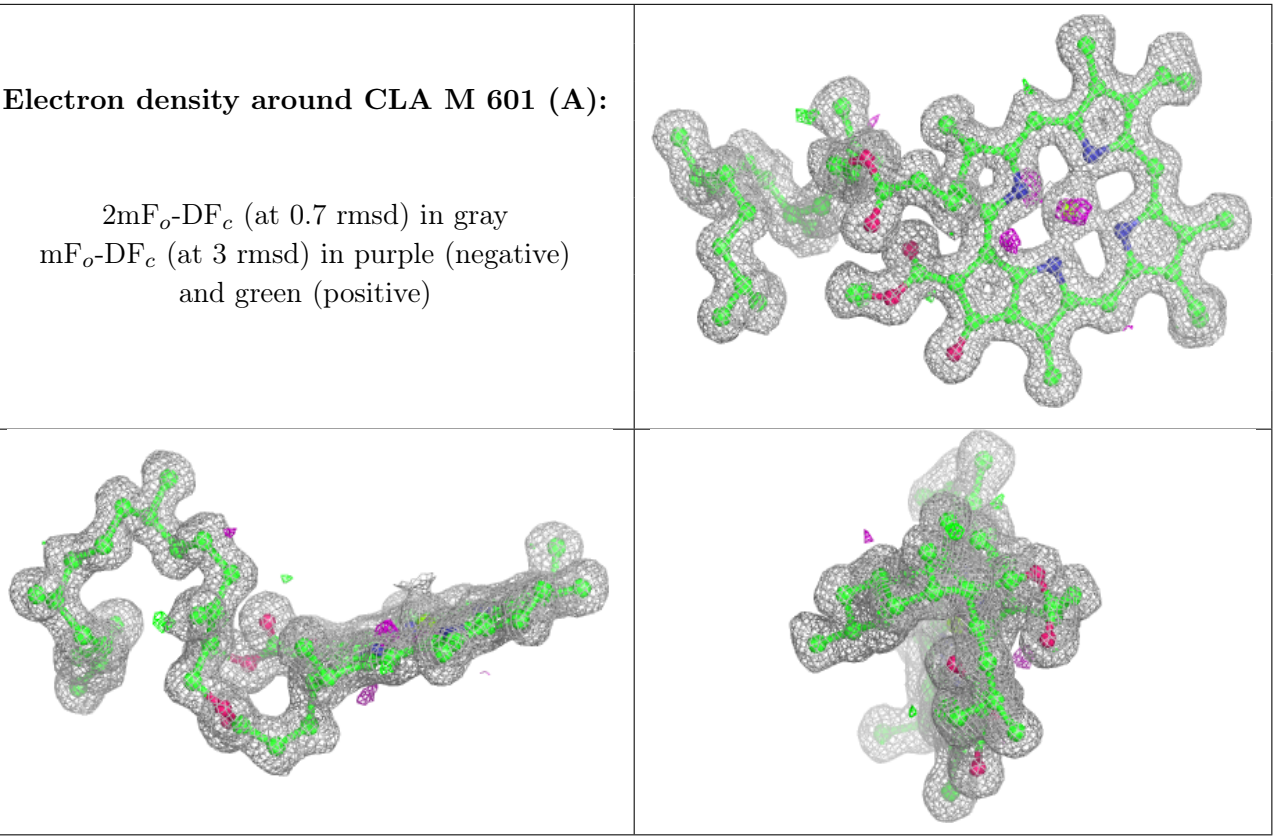
Electron density around PID M 612:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



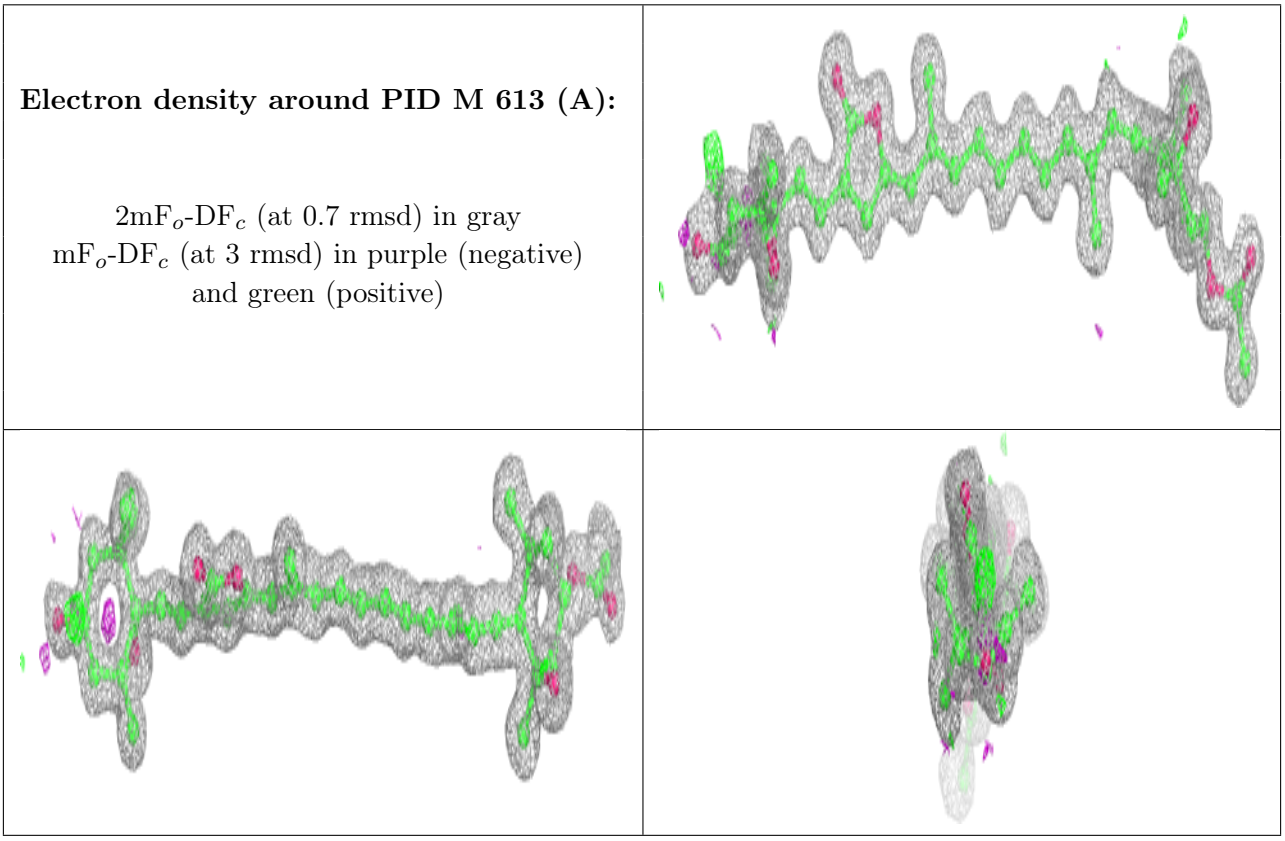
Electron density around CLA M 601 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



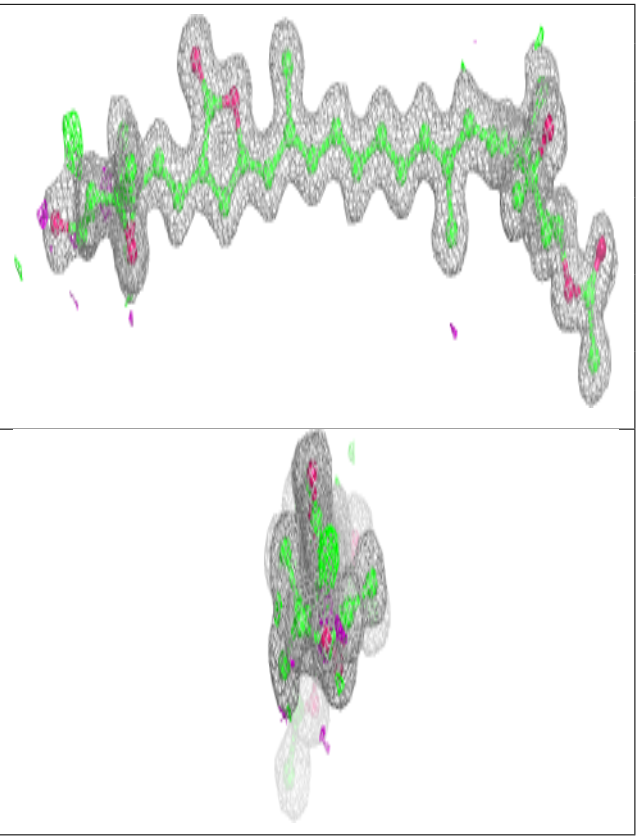
Electron density around PID M 613 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PID M 613 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PID M 614:

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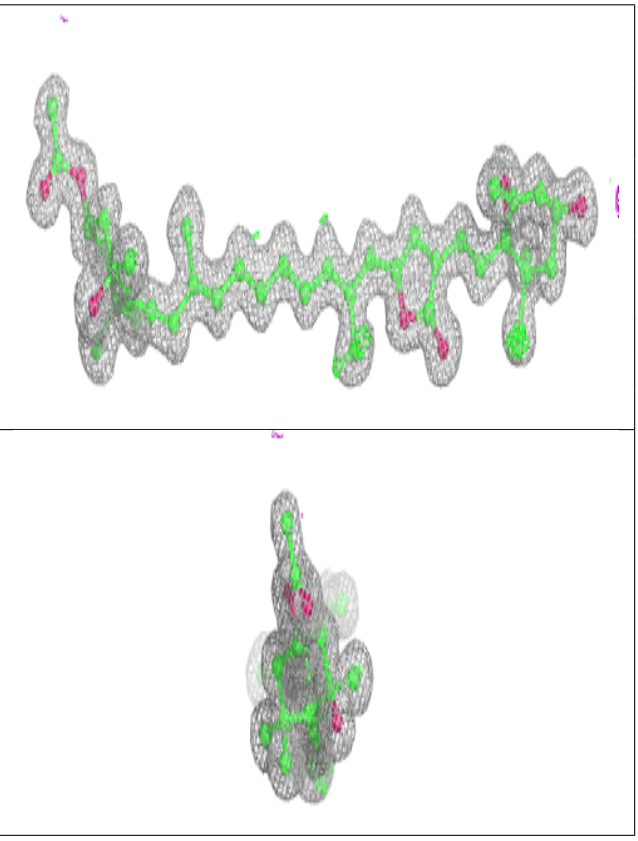
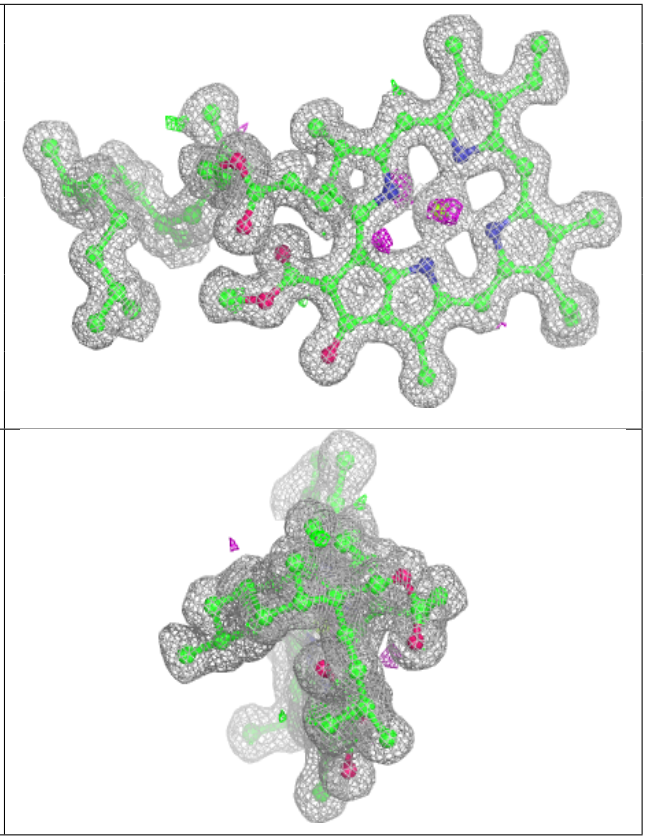
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



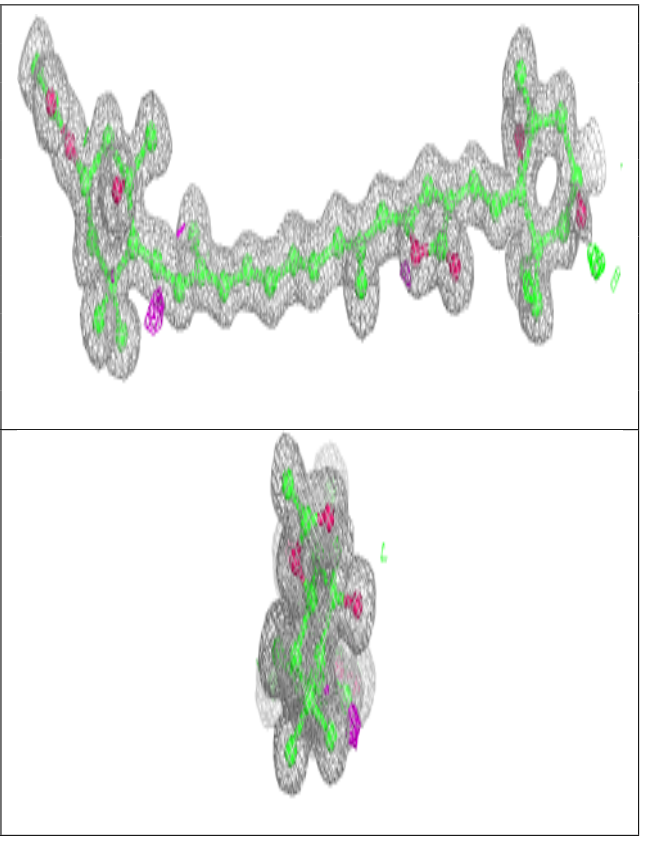
Electron density around CLA M 601 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



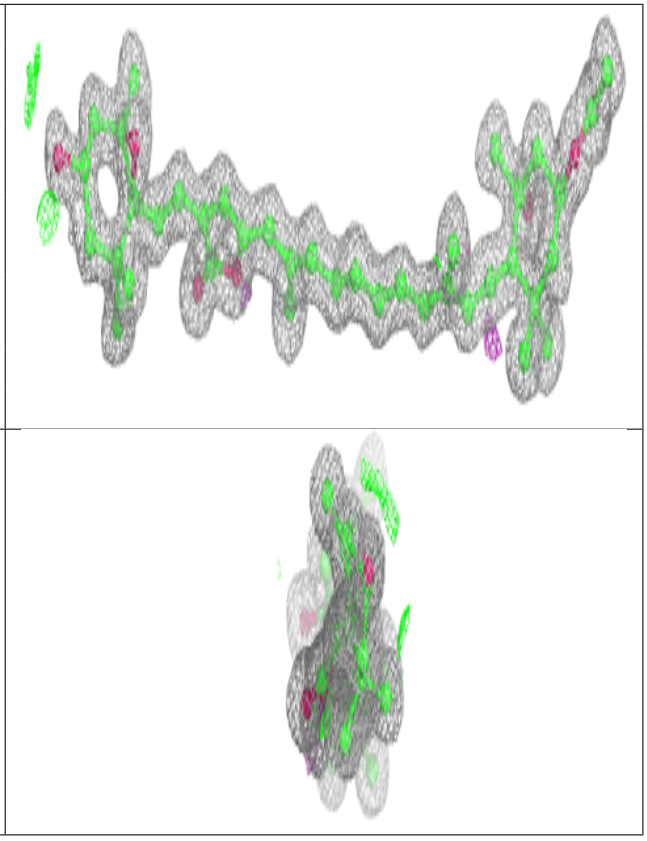
Electron density around PID M 611 (A):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around PID M 611 (B):

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.